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Dear Aaron:

I was very glad to get your long letter and the draft of your paper, but I had only time before the meeting to study them roughly and, as you probably heard from John, I developed a virus infection during the meeting so that it is only now that I have had the opportunity to go over it carefully.

My only strong criticism is on a rather detailed point. As I told John, you have no evidence at all that the number of base-pairs per superhelical turn is exactly 80. It could just as easily be 78 1/2 or 82. Even the evidence that it is near 80 is weak and indirect, though probably correct.

To take up a point in your letter, I am still not happy about the Stokes diameter. Ken van Holde is a very careful and capable physical chemist. Also he told me recently that his value at 105Å appears to be that for core nucleosomes. Of course, it is not reasonable to consider the particle a true elipsoid of 110x110x57. What one would like to know is, if the platysome is a cylinder of 110x110xh, what value of h gives a Stokes diameter of 105? There is no need to worry about hydration, since this is taken care of by this approach. Of course the platysome is hydrated. What we want to know are its exterior dimensions and shape. It is these which fix the so-called Stokes diameter. In short, can your X-ray dimensions, taken from the crystal, be made to fit the hydrodynamic measurements made in solution? Unfortunately I have forgotten if good theoretical figures are available for the drag of rather stubby cylinders, but I expect someone has either calculated it or measured it. However, this is all rather fussing about details since I have little doubt that the platysome 'height' is in the region of, say, 60Å rather than 100Å. Incidently when a crystal dries, what exactly does the C axis shorten to? Or is this impossible to measure?

My main criticism of your paper is that it is written 'historically' rather than logically. If you really have single crystal data for intact

cores, these should come first. Then the existence of clipped cores and the details of their unit cell. Then a companion of the two unit cells, using the X-ray powder data as well. Then the method of determining the phases of the three projections of the larger cell, using the e/m data. Next the three Fouriers so obtained and finally their interpretation, taking account of the density of the crystals.

All the other arguments, about the sinusoidal density variation and the distribution of the strong and weak reflections are irrelevant (even if they were very relevant historically) since they are automatically incorporated in the Fourier projections, except, of course, for reflections of the form hke (h,k,e, = 0), but as far as I can see none of these entered into your considerations.

About the discussion. No, I should not get involved with arguments about ΔL. I did mention Michael Levitt's work briefly at the meeting and was asked to write up my remarks in a slightly expanded form. I shall be sending a copy to Michael shortly. In your paper I suggest you ignore the whole topic.

Two small points. You really should refer to the Russian crystals in your introduction (John, to my embarrassment, omitted to mention them at the beginning of his talk). Also, I think you should refer briefly in the discussion to the work of Pardon et al., which was also presented at the Symposium here (and also in London?) or you will cause unnecessary ill-feeling.

John will have told you about most of the papers in the meeting. Also about the nice e/m pictures by Hans Ris of soleroids from Triturus erythrocytes. I could go on for pages about possible structures for solenoids, but I think it had better wait 'till we meet in August. Incidentally, Bak gave quite a sensible paper (after a little coaching!). They have quite nice data on Drosophila and also claim to have measured both the DNA and the mass, per unit length, of their 'unit fibre.'

We plan to return to LaJolla on the 1st of July, so do let me know how things are developing.